<110> HANMI PHARM. IND. CO., LTD.

<120> IgG Fc FRAGMENT FOR A DRUG CARRIER AND METHOD FOR THE PREPARATION THEREOF

<130> Q115525

<140> 10/535,341
<141> 2006-06-09

<150> PCT/KR04/02942
<151> 2004-11-13

<150> KR 10-2003-0080299
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<210> 1
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<220>
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<400> 1
cgtcatgccc agcacctgag ttcctggggg gacca 35

<210> 2
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 2
gggggatcct catttaccca gagacaggga gaggctcttc tg 42

<210> 3
<211> 12
<212> PRT
<213> Homo sapiens

<400> 3
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1 5 10

<210> 4
<211> 663
<212> DNA
<213> homo sapiens

<400> 4
tcatgcccag cacctgagtt cctgggggga ccatcagtct tcctgttccc cccaaaaccc 60

aaggacactc tcatgatctc ccggacccct gaggtcacgt gcgtggtggt ggacgtgagc 120

caggaagacc ccgaggtcca gttcaactgg tacgtggatg gcgtggaggt gcataatgcc 180

aagacaaagc cgcgggagga gcagttcaac agcacgtacc gtgtggtcag cgtcctcacc 240

gtcctgcacc aggactggct gaacggcaag gagtacaagt gcaaggtctc caacaaaggc 300

ctcccgtcct ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agagccacag 360

gtgtacaccc tgcccccatc ccaggaggag atgaccaaga accaggtcag cctgacctgc 420

ctggtcaaag gcttctaccc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 480

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 540

agcaggctaa ccgtggacaa gagcaggtgg caggagggga atgtcttctc atgctccgtg 600

atgcatgagg ctctgcacaa ccactacaca cagaagagcc tctccctgtc tctgggtaaa 660

tga 663

<210> 5
<211> 69
<212> DNA
<213> homo sapiens

<400> 5
atgaaaaaga caatcgcatt tcttcttgca tctatgttcg ttttttctat tgctacaaat 60

gcccaggcg 69

<210> 6
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
tctattgcta caaatgccca ggccttccca accattccct tatcc 45

<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
agataacgat gtttacgggt ccggaagggt tggtaaggga atagg 45

<210> 8
<211> 220

<212> PRT
<213> homo sapiens

<400> 8
Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
  1   5   10   15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            20   25   30

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
        35   40   45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    50   55   60

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65   70   75   80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                85   90   95

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
            100   105   110

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
        115   120   125

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    130   135   140

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
145   150   155   160

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                165   170   175

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
            180   185   190

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        195   200   205

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    210   215   220

<210> 9
<211> 654
<212> DNA
<213> homo sapiens

<400> 9
gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact   60

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac   120

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag   180

ccgcgggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac   240

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc   300

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 360

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 420

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 480

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 540

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 600

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggtaa atga 654

<210> 10
<211> 217
<212> PRT
<213> homo sapiens

<400> 10

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Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
  1               5                  10                  15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
    210                 215
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<210> 11

<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
cgccgtgccc agcacctgaa ctcctggggg gac 33

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 12
gggggatcct catttacccg gagacaggga gag 33

<210> 13
<211> 15
<212> PRT
<213> homo sapiens

<400> 13
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 14
<211> 660
<212> DNA
<213> homo sapiens

<400> 14
ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 60

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 120

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 180

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 240

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 300

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agagccacag 360

gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 420

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 480

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 540

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 600

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 660

<210> 15
<211> 220
<212> PRT
<213> homo sapiens

<400> 15
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
  1   5   10   15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            20   25   30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        35   40   45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    50   55   60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65   70   75   80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                85   90   95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            100   105   110

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
        115   120   125

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    130   135   140

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
145   150   155   160

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                165   170   175

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            180   185   190

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        195   200   205

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210   215   220

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
cggcacctga actcctgggg ggaccg   26

<210> 17
<211> 651
<212> DNA
<213> homo sapiens

<400> 17
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 60

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 120

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 180

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 240

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 300

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 360

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 420

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 480

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 540

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 600

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a   651

<210> 18
<211> 217
<212> PRT
<213> homo sapiens

<400> 18
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
  1   5   10   15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35   40   45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100   105   110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115   120   125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130   135   140

```
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215


<210>    19
<211>    29
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    primer


<400>    19
cgccgtgccc agcacctccg gtggcggga                                        29


<210>    20
<211>    33
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    primer


<400>    20
gggggatcct catttacccg gagacaggga gag                                   33


<210>    21
<211>    12
<212>    PRT
<213>    homo sapiens

<400>    21
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
  1               5                  10


<210>    22
<211>    657
<212>    PRT
<213>    homo sapiens

<400>    22
Cys Cys Gly Thr Gly Cys Cys Cys Ala Gly Cys Ala Cys Cys Thr Cys
  1                 5                  10                  15

Cys Gly Gly Thr Gly Gly Cys Gly Gly Gly Ala Cys Cys Gly Thr Cys
             20                  25                  30
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Ala Gly Thr Cys Thr Thr Cys Cys Thr Cys Thr Thr Cys Cys Cys Cys
          35                  40                  45

Cys Cys Ala Ala Ala Ala Cys Cys Cys Ala Ala Gly Gly Ala Cys Ala
      50                  55                  60

Cys Cys Cys Thr Cys Ala Thr Gly Ala Thr Cys Thr Cys Cys Cys Gly
 65                  70                  75                  80

Gly Ala Cys Cys Cys Cys Thr Gly Ala Gly Gly Thr Cys Ala Cys Ala
                 85                  90                  95

Thr Gly Cys Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Cys Gly
            100                 105                 110

Thr Gly Ala Gly Cys Cys Ala Cys Gly Ala Ala Gly Ala Cys Cys Cys
        115                 120                 125

Thr Gly Ala Gly Gly Thr Cys Cys Ala Gly Thr Thr Cys Ala Ala Cys
    130                 135                 140

Thr Gly Gly Thr Ala Cys Gly Thr Gly Gly Ala Cys Gly Gly Cys Gly
145                 150                 155                 160

Thr Gly Gly Ala Gly Gly Thr Gly Cys Ala Thr Ala Ala Thr Gly Cys
                165                 170                 175

Cys Ala Ala Gly Ala Cys Ala Ala Ala Gly Cys Cys Gly Cys Gly Gly
            180                 185                 190

Gly Ala Gly Gly Ala Gly Cys Ala Gly Thr Thr Thr Ala Ala Cys Ala
        195                 200                 205

Gly Cys Ala Cys Gly Thr Thr Thr Cys Gly Thr Gly Thr Gly Gly Thr
    210                 215                 220

Cys Ala Gly Cys Gly Thr Cys Cys Thr Cys Ala Cys Cys Gly Thr Cys
225                 230                 235                 240

Gly Thr Gly Cys Ala Cys Cys Ala Gly Gly Ala Cys Thr Gly Gly Cys
                245                 250                 255

Thr Gly Ala Ala Thr Gly Gly Cys Ala Ala Gly Gly Ala Gly Thr Ala
            260                 265                 270

Cys Ala Ala Gly Thr Gly Cys Ala Ala Gly Gly Thr Cys Thr Cys Cys
        275                 280                 285

Ala Ala Cys Ala Ala Ala Gly Gly Cys Cys Thr Cys Cys Cys Ala Gly
    290                 295                 300

Cys Cys Cys Cys Cys Ala Thr Cys Gly Ala Gly Ala Ala Ala Ala Cys
305                 310                 315                 320

Cys Ala Thr Cys Thr Cys Cys Ala Ala Ala Ala Cys Cys Ala Ala Ala
                325                 330                 335

Gly Gly Gly Cys Ala Gly Cys Cys Cys Cys Gly Ala Gly Ala Gly Cys
            340                 345                 350

Cys Ala Cys Ala Gly Gly Thr Gly Thr Ala Cys Ala Cys Cys Cys Thr
        355                 360                 365
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Gly Cys Cys Cys Cys Cys Ala Thr Cys Cys Cys Gly Gly Gly Ala Ala
    370                 375                 380

Gly Ala Gly Ala Thr Gly Ala Cys Cys Ala Ala Gly Ala Ala Cys Cys
385                 390                 395                 400

Ala Gly Gly Thr Cys Ala Gly Cys Cys Thr Gly Ala Cys Cys Thr Gly
                405                 410                 415

Cys Cys Thr Gly Gly Thr Cys Ala Ala Ala Gly Gly Cys Thr Thr Cys
            420                 425                 430

Thr Ala Thr Cys Cys Cys Ala Gly Cys Gly Ala Cys Ala Thr Cys Gly
        435                 440                 445

Cys Cys Gly Thr Gly Gly Ala Gly Thr Gly Gly Gly Ala Gly Ala Gly
    450                 455                 460

Cys Ala Ala Thr Gly Gly Gly Cys Ala Gly Cys Cys Gly Gly Ala Gly
465                 470                 475                 480

Ala Ala Cys Ala Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys Ala
                485                 490                 495

Cys Gly Cys Cys Thr Cys Cys Cys Ala Thr Gly Cys Thr Gly Gly Ala
            500                 505                 510

Cys Thr Cys Cys Gly Ala Cys Gly Gly Cys Thr Cys Cys Thr Thr Cys
        515                 520                 525

Thr Thr Cys Cys Thr Cys Thr Ala Cys Ala Gly Cys Ala Ala Gly Cys
    530                 535                 540

Thr Cys Ala Cys Cys Gly Thr Gly Gly Ala Cys Ala Ala Gly Ala Gly
545                 550                 555                 560

Cys Ala Gly Gly Thr Gly Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly
                565                 570                 575

Ala Ala Cys Gly Thr Cys Thr Thr Cys Thr Cys Ala Thr Gly Cys Thr
            580                 585                 590

Cys Cys Gly Thr Gly Ala Thr Gly Cys Ala Thr Gly Ala Gly Gly Cys
        595                 600                 605

Thr Cys Thr Gly Cys Ala Cys Ala Ala Cys Cys Ala Cys Thr Ala Cys
    610                 615                 620

Ala Cys Gly Cys Ala Gly Ala Ala Gly Ala Gly Cys Cys Thr Cys Thr
625                 630                 635                 640

Cys Cys Cys Thr Gly Thr Cys Thr Cys Cys Gly Gly Gly Thr Ala Ala
                645                 650                 655

Ala
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<210> 23
<211> 219
<212> PRT
<213> homo sapiens

<400> 23
Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
 1   5   10   15

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
            20   25   30

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
        35   40   45

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
    50   55   60

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
65   70   75   80

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                85   90   95

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
            100   105   110

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
        115   120   125

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
    130   135   140

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
145   150   155   160

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
                165   170   175

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
            180   185   190

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
        195   200   205

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210   215

<210> 24
<211> 10
<212> PRT
<213> Homo sapiens

<400> 24
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 1   5   10

<210> 25
<211> 10
<212> PRT
<213> Homo sapiens

<400> 25
Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly
 1   5   10

<210> 26
<211> 10
<212> PRT
<213> Homo sapiens

<400> 26
Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
  1   5   10